

Figure 1A

1	ATGACAACTCTTGTCTGC	AAACCCTCCTCC	TCTCTCTG	GACCC	TGCCAGGGCAG		60		
1	M T T L V P A T L S F	L L L W T L P G Q				20			
61	GTCCCTCTCAGGGTGGC	CCTGGCAAAGAGGA	ACTCAAATCTGG	AACCAAGGGTCCCAG		120			
21	V L L R V A L A K E	E E V K S G T K G S Q				40			
121	CCCATGTCCCCCTCTGAT	TCTAGACAAACTATGGG	GCAACATCTGG	ATATGATGATGCC		180			
41	P M S P S D F L D K L M G R T S G Y D A					60			
181	AGGATT CGGCCAATT	TAAGGCCAACCGT	GAACGTGACCTG	CAACATCTTCATCAAC		240			
61	R I R P N F K G P P V N V T C N I F I N					80			
241	AGTTT CAGCTCCG	TACCAAGACCA	AACTGGACTAC	CGGTGAATGTC	TCTGGGCAA		300		
81	S F S S V T K T T M D Y R V N V F L R Q					100			
301	CAGTGGAAATGACCC	ACGCC	ACGCC	TGCTCACCG	GAGAATATCCTGATGACT	TCTGGACCTCGAT		360	
101	Q W N D P R L S Y R E Y P D D S L D L D					120			
361	CCCTCCATGCTGGACT	TATCTGGAAAGCC	AGACGCTTCTTG	CTAATGAGAAAGGGC		420			
121	P S M L D S I W K P D L F F A N E K G A					140			
421	AACTCCATGAGGTGAC	CAACGGACAACAAGT	TACTGCGC	ATCTTC	CAAGAATGGGAATGTG		480		
141	N F H E V T T D N K L L R I F K N G N V					160			
481	CTGTACAGCATCAGG	CTGACCC	CTCATT	TGTCTG	CCGTGATGGACCTCAAGAA	ACTTCCCC		540	
161	L Y S I R L T L I L S C L M D L K N F P					180			
541	ATGGACATCCAGAC	CTGCA	CGATGCG	CTTGAGAGCTT	GGCTACACCATGAAAGACCTC		600		
181	M D I Q T C T M Q L E S					200			
601	GTGTTTGAGTGGCTGG	AAAGATGCT	CTGCTG	TCAGG	CTGAGGGCTGACTCTGCC		660		
201	V F E W L E D A P A V Q V A E G L T L P					220			
661	CAGTTTATCTTGCGGG	ATGAGAAGGATCT	AGGTGTTG	TACCAAGC	ACTACAACACAGGG		720		
221	Q F I L R D E K D L G C C T					240			
721	AAATT CACCTGCATCGAGG	TAAAGTTCAC	CTGGACGGCAGATGGG	CTACTATCTGATT		780			
241	K F T C I E V K F H L E R Q M G Y Y L I					260			
781	CAGATGTACATCCCAGC	TACTCATCGTC	ATCCTG	TGGCTCCTCTG	GATCAAC		840		
261	Q M Y I P S L L I V I L S W V S F W I N					280			
841	ATGGATGCTGCCCTGCC	GCTGGG	CTGGGCATCAC	ACCCGGT	GCTCACCATGACCA		900		
281	M D A A P A R V G L G I T T V L T M T T					300			

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Figure 1B

901	CAGAGCTCTGGCTCCGGGCCTCTTGCTTAAGGTGCTTACGTGAAGGCAATCGACATC	960
301	<u>Q S S G S R A S L P K V S Y V K A I D I</u>	320
961	TGGATGGCTGTGTGCTGCTCTTTGTGTTGCTGCCCTGCTGGAGTATGCTGCCATAAAT	1020
321	<u>W M A V C L L F V F A A L L E Y A A I N</u>	340
1021	TTTGTTCCTCGTCAGCATAAAAGATTACAGACTTCGAAGAAGGCAGAGGCGCCAACGC	1080
341	<u>F V S R Q H K E F I R L R R R Q R R Q R</u>	360
1081	TTGGAGGAAGATATCATCCAAGAAAGTCGTTCTATTTCCGTGGCTATGGCTGGCAC	1140
361	L E E D I I Q E S R F Y F R G Y G L G H	380
1141	TGCTGCAGGCAAGAGATGGAGGTCCAATGGAAAGGTTCTGGCATTTATAGTCCCCAACCT	1200
381	C L Q A R D G G P M E G S G I Y S P Q P	400
1201	CCAGCCCCCTTCTAAGGGAAGGAGAAACCACCGGAAACTCTACGTGGACTGAGCCAAG	1260
401	P A P L L R E G E T T T R K L Y V D	417
1261	AGAATTGACACCATCTCCGGGCTGTCCTCCCTTCACCTTCCTCATCTCAATATCTTC	1320
1321	TACTGGGTTGTCTATAAGTGCTACGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGG	1380
1381	TGGGAGCTATAGAGTCTGCTGGCTGGCCCTCTGCTCCCTGGTGGCTTCTCCCTC	1440
1441	AGTTAGACTCCATTAGGGTTGGACAGTCTCCCTGTATCTCCACTCAGAACTTCAAC	1500
1501	TACCAAGTCCCAAAGCTATGGGCCTATATTGCATGGTGCCTGACTTATA	1560
1561	AAGATGGCTTATCTACCCCTAGTCATATTCTCCATACTTCCATTCTCATGAGACT	1620
1621	AAGGTTGGCACATTCCCTGGGCCAGGATGACCTTCTGCCCTGGCTGGACCTCCCTGT	1680
1681	TTTCCAATACTCCAGTGGAGAGTATTCAAGAACACTGCTGCTAGATTCTGGCATTGT	1740
1741	CTTAATCTGCACCACTCTCCCCCTGCCACCTCCCAGAGGCCATTACTCTGT	1800
1801	CCTCTGTCCCTCTGCTGCAAGATTCAAATGGTAGTTCTCTATCCACAAGTGTGCC	1860
1861	TGTGGGGCTAGTCAGGTTCTTGAGAGTGAAGAGGAAAGCCGAAAGTCCCCACC	1920
1921	TCTCGAGAGGGTTGAAACAGTCATAGGCTGCACTGGCTAGCGACTATATGGCCAAACAG	1980

Figure 1C

1981 AGAGGTGTTCAAGTCTTGGGAAGCCCCACACTTGCTTCATCCCTTCTATTGCG 2040
2041 CTTGTCTGCTTTCTGTCACTGAGATACTCCTTGTCTGTCTTAGTTGAGGA 2100
2101 GAGCGTTCTGAGCTGACCAGGGTAGCTGGTCAGAAATTACTGTCAGAATTGGGGCAGAG 2160
2161 ACTTTGGGTTCTCAAAAAGACTAACCTCCAGATCCACCTGAACATTCTGGTCTCAGAAA 2220
2221 TATTGTTCCGTTCCCTAATTAACCTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGAG 2280
2281 TGTAAAAAAAGAAAAAACTTGTTCTTAAGAAACTTACTTATGATGCTAGAAAACTTT 2340
2341 TGAGAAAAGTAGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAAATAGAGAAAATATTCT 2400
2401 CAGAGTGCTTTGTTGGCTGGCTTCATTGTTCTTCTCACCAAAGTCTATT 2460
2461 TCCAGGGCCCTCATTCCAACCTGGCTTCAACCTCCTTGGTGTGCAAATAAGGTG 2520
2521 CCGCTGCAACCTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAA 2565

1000 900 800 700 600 500 400 300 200 100

Figure 2A

1	ATGACAACTCTTGTCTGCACCCCTCCTTCCTCTGGACCCGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCCTCCTCAGGGTGGCCTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTTCTAGACAAACTTATGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTGGCCCAATTAAAGGCCACCCGTGAACGTGACCTGCAACATCTTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCGTCACCAAGACCACATGGACTACCGGGTGAATGTCCTTGGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCCCTGTCTACCGAGAATATCCTGATGACTCTCTGGACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGGCCAGACCTCTTGCTTAATGAGAAAGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTCAAGAATGGGAATGTC	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCTCATTGCTGCTGATGGACCTCAAGAACTTCCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACGTGCACGATGCGAGCTTGAGAGCTCATCCATACTCTGCAGCCCTCTG	600
181	M D I Q T C T M Q L E S S S I L C S P L	200
601	CCATCTCTGACTTTCAGTTGGCTACACCATGAAAGACCTCTGTTGAGTGGCTGGAA	660
201	P S L S L S V [REDACTED] T M K D L V F E W L E	220
661	GATGCTCCTGCTGTCCAAGTGGCTGAGGGGCTGACTCTGCCAGTTATCTGGGGAT	720
221	D A P A V Q V A E G L T L P Q F I L R D	240
721	GAGRAGGATCTAGGCTGTTGATCRAAGCACTACAAACACAGGGAAATTCACTGCATCGAG	780
241	E K D L G C C T [REDACTED] G K F T C I E	260
781	GTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATTGAGATGACATCCCCAGC	840
261	V K F H L E R Q M G Y Y L I Q M Y I P S	280
841	CTACTCATCGTCATCCTGCTGGCTCCTCTGGATCAACATGGATGCTGCCCTGCC	900
281	L L I V I L S W V S F W I N M D A A P A	300

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Figure 2B

901	CGTGTGGGCCTGGGCATCACCAACCGTGCCTACCATGACCACCCAGAGCTCTGGCTCCCGG	960
301	R <u>V</u> G L G I T T V L T M T T Q S S G S R	320
961	GCCCTTTGCCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTC	1020
321	A S L P K V S Y V K A I D <u>I</u> W M A V C L	340
1021	CTCTTGTTGCTCGCTGCCCTGCTGGAGATATGCTGCCATAAAATTGTTCTCGTCAGCAT	1080
341	<u>L</u> F V F A A L L E Y A A I N F V S R Q H	360
1081	AAAGAATTCATACGACTTGAAGAAGGCAGAGGCAGCAACGCTTGGAGGAAGATATCATC	1140
361	K E F I R L R R Q R R Q R L E E D I I	380
1141	CAAGGAAAGTCGTTCTATTCCGTGGCTATGGCTTGGGCCACTGCCTGCAGGCAGAGAT	1200
381	Q E S R F Y F R G Y G L G H C L Q A R D	400
1201	GGAGGTCCAATGGAAGGTCTGGCATTATAGTCCCCAACCTCCAGCCCCCTTCTAAGG	1260
401	G G P M E G S G I Y S P Q P P A P L L R	420
1261	GAAGGAGAACACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC	1320
421	E G E T T R K L Y V D	431
1321	CGGGCTGTCTCCCTTCACTTCCTCATCTCAATATCTTCACTGGGTGTCTATAAA	1380
1381	GTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGAGCTATAGAGTCCT	1440
1441	GCTGCTGGCCTCCTGCTTCCCTCTGGTGGCTTCTCCCTCAGTTAGACTCCATTAGGG	1500
1501	GTTTGGACAGTTCCTTCCGTATCTCCACTCAGAACTTCAACTACCAGTCCAAAGCTAT	1560
1561	GTGGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC	1620
1621	TAAAAAAAAAAAAAAA	1640

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Figure 3A

	1	50
GRA1_HUMAN	(1) -----MYSFNTLRLIHLSGALIVFLSLAAEKFATRSATAKPMSPSDFLDK	
GRA3_HUMAN	(1) -MAHVRHRFLBLSGCTTWEAALLLSLVAKTEISAKERSAPMSDFLDK	
HGRA4	(1) MTTLVPATLFLLLTLPGQVLLRVALAKEEVKGSKLGKQPMSPSDFLDK	
HGRA4sv	(1) MTTLVPATLFLLLTLPGQVLLRVALAKEEVKGSKLGKQPMSPSDFLDK	
GRA4_MOUSE	(1) -----VALAKEDGKSLKGKQPMSPSDFLDK	
GRA2_HUMAN	(1) MNQCVNILLALDAPLETNHRTCPCKDHSSESGKQPSQSPSDFLDK	
	51	100
GRA1_HUMAN	(45) LMGRTSGYDARIRPNFKGPPVNVCNFIFNSCGSTETTMDYRVNFLRQ	
GRA3_HUMAN	(50) LMGRTSGYDARIRPNFKGPPVNTCNFIFNSCGSTETTMDYRVNFLRQ	
HGRA4	(51) LMGRTSGYDARIRPNFKGPPVNTCNFIFNSCGSTETTMDYRVNFLRQ	
HGRA4sv	(51) LMGRTSGYDARIRPNFKGPPVNVCNFIFNSCGSTETTMDYRVNFLRQ	
GRA4_MOUSE	(27) LMGRTSGYDARIRPNFKGPPVNTCNFIFNSCGSTETTMDYRVNFLRQ	
GRA2_HUMAN	(51) LMGRTSGYDARIRPNFKGPPVNTCNFIFNSCGSTETTMDYRVNFLRQ	
	101	150
GRA1_HUMAN	(95) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
GRA3_HUMAN	(100) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
HGRA4	(101) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
HGRA4sv	(101) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
GRA4_MOUSE	(77) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
GRA2_HUMAN	(101) QNNDPRLIYEYFPDDSLDLDPMSMLDSIWKPDLEFFANEKGQNFHEVITDNK	
	151	200
GRA1_HUMAN	(145) LLRKFGNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
GRA3_HUMAN	(150) ILFRFKNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
HGRA4	(151) LRLKFGNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
HGRA4sv	(151) LRLKFGNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
GRA4_MOUSE	(127) LRLKFGNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
GRA2_HUMAN	(151) LRLKFGNGNVLYSIRTLILQLCPMDLKNFPMDFQTCIMQLES-----	
	201	250
GRA1_HUMAN	(187) -----EGYTMDLIFENQEEGA-QVQVGLTLPQFILNEENDLRYCTKH	
GRA3_HUMAN	(192) -----EGYTMDLIFENQEEGA-QVQVGLTLPQFILNEENDLRYCTKH	
HGRA4	(193) -----EGYTMDLIFENQEEGA-QVQVGLTLPQFILNEENDLGCCTKH	
HGRA4sv	(201) PSLSLSVGYTMIDIFENQEEGA-QVQVGLTLPQFILNEENDLGCCTKH	
GRA4_MOUSE	(169) -----EGYTMDLIFENQEEGA-QVQVGLTLPQFILNEENDLGCCTKH	
GRA2_HUMAN	(193) -----EGYTMDLIFENQEEGA-QVQVGLTLPQFILNEENDLGCCTKH	
	251	[<<<<<<<TM1>>>>>>] 300
GRA1_HUMAN	(230) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
GRA3_HUMAN	(235) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
HGRA4	(237) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
HGRA4sv	(251) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
GRA4_MOUSE	(213) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
GRA2_HUMAN	(236) YNTGKFTCIEVFHLERQMGYYLIQMYIPSLLIVLWSNSFWINMDAAP	
	3 [<<<<<<<TM2>>>>]	[<<<<<<<<<TM3
GRA1_HUMAN	(280) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	
GRA3_HUMAN	(285) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	
HGRA4	(287) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	
HGRA4sv	(301) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	
GRA4_MOUSE	(263) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	
GRA2_HUMAN	(286) RVGGLGTTVLMTTQSSGSRASLPKPVSYVAIKADIMWAVCLLFLVEALLEY	

Figure 3B

>>>>]

GRA1_HUMAN	(330)	AVNFVSRQKEFLRERRR-----	400		
GRA3_HUMAN	(335)	AVNFVSRQKEFLRERRRNNKTEAFALEKFYRFSDMDEA	RESRFSE		
HGRA4	(337)	AVN	FVSRQKEFLRERRR-----	RQRLEED	ESRFYFR
HGRA4sv	(351)	AVNFVSRQKEFLRERRR-----	RQRLEED	ESRFYFR	
GRA4_MOUSE	(313)	AVNFVSRQKEFLRERRR-----	RQR	-----	
GRA2_HUMAN	(336)	AVNFVSRQKEFLRERRR-----	RQKEED	RESRFNFS	
 401					
GRA1_HUMAN	(366)	YGGMGPACLQAKDGISVKGINNSNTPPPAPSKEPEENRKLF	450	RAKNI	
GRA3_HUMAN	(385)	YGGMGP-CLQAKDGMPKGDN-----	PVQVMPKPDPE	RKVF	DRAKNI
HGRA4	(375)	GYCIGH-CLQARDGPMIGS-CIYSPQQPAPL	NRGETTRKL	VD-----	-----
HGRA4sv	(389)	GYCIGH-CLQADGPMIGS-CIYSPQQPAPL	NRGETTRKL	VD-----	-----
GRA4_MOUSE	(338)	-----	-----	-----	-----
GRA2_HUMAN	(374)	GYGMGH-CLQKDGTAKKTPNPPLPQPK-----	GDA	KKFVDRAKNI	
 451					
GRA1_HUMAN	(416)	DKISRIGFPAAFLIFNIFYWITYKIEERHED	487	HNO-----	
GRA3_HUMAN	(429)	DTISRACFPAAFLIFNIFYWITYKIEERHED	HQQOD		
HGRA4	(418)	-----	-----	-----	
HGRA4sv	(432)	-----	-----	-----	
GRA4_MOUSE	(338)	-----	-----	-----	
GRA2_HUMAN	(419)	DTISRRAAPPAAFLIFNIFYWITYKIEERHED	HKK-----		

TOMOLOGY
STRUCTURE
FUNCTION

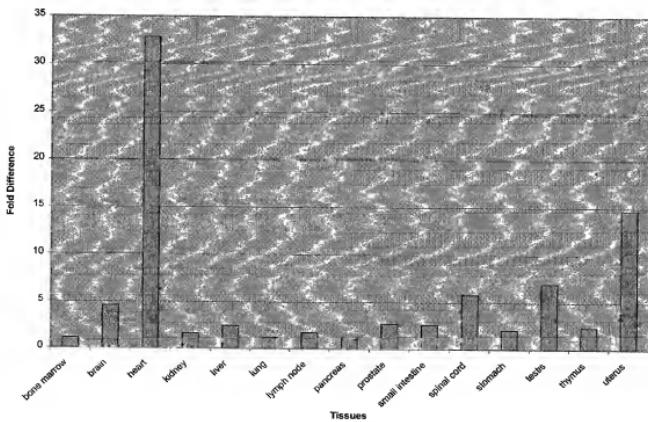
Figure 4

Figure 5

G1934909_001 MTTLVPATLSSLNLNTLPQGVLLRVALAKEEVKSGTKGSPMSPSDFLDKLMGRTSGYDA
cloneE3 MTTLVPATLSSLNLNTLPQGVLLRVALAKEEVKSGTKGSPMSPSDFLDKLMGRTSGYDA
cloneD8 MTTLVPATLSSLNLNTLPQGVLLRVALAKEEVKSGTKGSPMSPSDFLDKLMGRTSGYDA

G1934909_001 RIRPNFKGPVPNVTNCNIFINSFSSITKTTMACWAPGNGNVSEGPISAPSQDYRVNVFLRQ
cloneE3 RIRPNFKGPVPNVTNCNIFINSFSSITKTT-----DYZRVNVFLRQ
cloneD8 RIRPNFKGPVPNVTNCNIFINSFSSITKTT-----DYZRVNVFLRQ

G1934909_001 QWNNDPLLSYREYPPDSLDLDPSPMLSIIWKPDLFFANEKGANFHEVTTDNKLRLI FKGNV
cloneE3 QWNNDPLLSYREYPPDSLDLDPSPMLSIIWKPDLFFANEKGANFHEVTTDNKLRLI FKGNV
cloneD8 QWNNDPLLSYREYPPDSLDLDPSPMLSIIWKPDLFFANEKGANFHEVTTDNKLRLI FKGNV

G1934909_001 LYSIRLTLILSCLMDLKNFPMDIQCTCTMoles-----FGYTMKDLVFEWLE
cloneE3 LYSIRLTLILSCLMDLKNFPMDIQCTCTMoles-----FGYTMKDLVFEWLE
cloneD8 LYSIRLTLILSCLMDLKNFPMDIQCTCTMolesLESSILCSPLSLSVGXTM KDLVFEWLE

G1934909_001 DAPAVQVAEGLTLPCFILRDERKD LGCTKHYNTGKFTCIEVKFHLLERQMGYLYI QMViPS
cloneE3 DAPAVQVAEGLTLPCFILRDERKD LGCTKHYNTGKFTCIEVKFHLLERQMGYLYI QMViPS
cloneD8 DAPAVQVAEGLTLPCFILRDERKD LGCTKHYNTGKFTCIEVKFHLLERQMGYLYI QMViPS

G1934909_001 LLIVILSWVSFWINNMDAAPARVGLGITTVLMTTQS SGSRASLP-----
cloneE3 LLIVILSWVSFWINNMDAAPARVGLGITTVLMTTQS SGSRASLPKVSYVKAIDIWMAVCL
cloneD8 LLIVILSWVSFWINNMDAAPARVGLGITTVLMTTQS SGSRASLPKVSYVKAIDIWMAVCL

G1934909_001 LVFVAALLEYAAINFVSROHKEFIRLRRQRQRLEEDI I QESRFYFRGYGLGHCLQARD
cloneE3 LVFVAALLEYAAINFVSROHKEFIRLRRQRQRLEEDI I QESRFYFRGYGLGHCLQARD
cloneD8 LVFVAALLEYAAINFVSROHKEFIRLRRQRQRLEEDI I QESRFYFRGYGLGHCLQARD

G1934909_001 -----
cloneE3 GGMMEGSGIYSPCPPAPLRLREGETTRKLYVD
cloneD8 GGMMEGSGIYSPCPPAPLRLREGETTRKLYVD

Figure 6.**HGRA4**

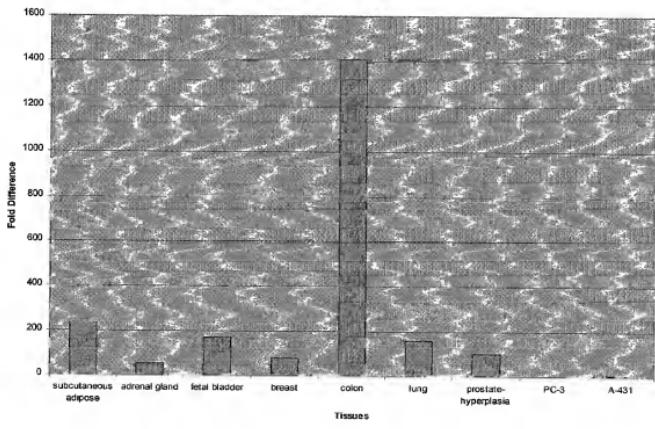
<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

HGRA4sv

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

Figure 7

Figure 8



202720: 91852007

Figure 9

